

Figure 1

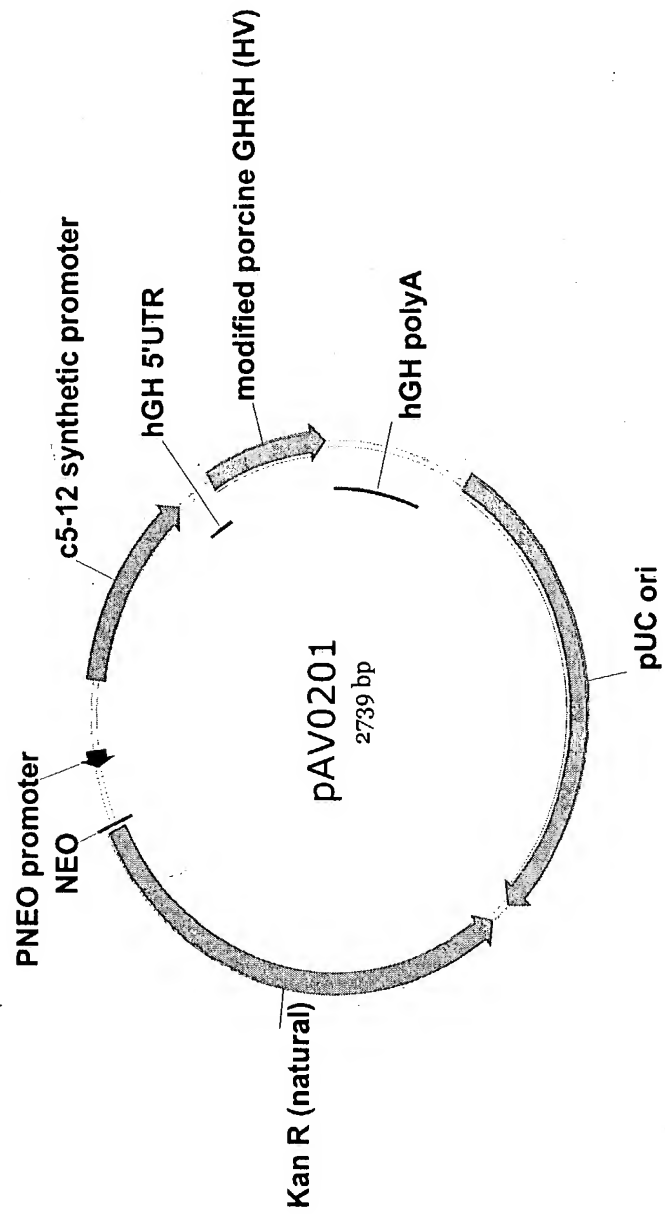


Figure 2

1 M I E Q D G L H A G S P A A W V E R L F G Y D W A Q Q T I G C S D A .
 ATGATTGAC AAGATGATT GCAAGCAGT TCTCGGCGG CTGTGGTGA GAGGTATTC GGCTATGACT GGGCAACA GACATCGG TGCTCTGATG
 TACTACTTG TTCTACTAA CGTGGTCCA AGAGCGGGG GAACCCACT CTCCGATAG CCATATGTA CCGGTGTTGT CTGTAGCCG ACAGACTAC
 . A V F R L S A Q G R P V L F V K T D L S G A L N E L Q D E A A R L .
 301 CCGCGTGT CCGCTGTCA GCGCAGGGG GCCCGTTCT TTTGTCAAG ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGGGGT
 GCGGCACAA GCGGACAGT CCGGTCCCG CCGGCCAAGA AAAACAGTTC TGGTGGACA GGCACGGA CTACTTGAC GTCTGTCTCC GTCGSCCGA
 . S W L A T T G V P C A A V L D V V T E A G R D W L L L G E V P G Q
 201 ATCGTGGTG GCCACGACG GGTTCCTTG CCGAGCTGTG CTCGACGTTG TCACTGAAGC GGGAAAGGAC TGCTGTCTAT TGGCGAAGT GCCGGGCGAG
 TAGCACCGAC CCGTGTCTGC CGCAAGGAAC CCGTCGACAC GAGCTGCAAC AGTGACTTCG CCCTTCCCTG ACCGACGATA ACCGCTTCA CCGCCCCGTC
 D L L S S H L A P A E K V S I M A D A M R R L H T L D P A T C P F D .
 301 GATCTCTGT CATCTACCT TGCTCTGCG GAGAAAGTAT CCATCATGGC TGATGCAATG CCGCGGCTGC ATACGCTTGA TCGGCTACC TGCCCATTCG
 CTAGAGGACA GTAGAGTGA ACGAGACGG CTCCTTCATA GGTAGTACCG ACTAGTTAC GCGCCGACG TATGCGAAT AGGCCGATGG ACGGTAAGC
 . H Q A K H R I E R A R T R M E A G L V D Q D D L D E E H Q G L A P .
 401 ACCACCAAGC GAAACATGC ATCGAGCGAG CACGTACTCG GATGGAAGC GGTCTGTG ATCAGATGA TCTGGACGAA GAGCATCAGG GGTCTCGGCC
 TGGTGGTTCG CTGTGTAGCG TAGCTCGTC GTGCATGAGC CTACCTTGG CCAGAACAGC TAGTCTACT AGACCTGCTT CTCGTAGTCC CCGAGCGCGG
 . A E L F A R L K A R M P D G E D L V V T H G D A C L P N I M V E N
 501 AGCGAATG TCGCCAGG TCAAGCGG CATGCCGAC GCGAGGATC TGTGCTGAC TCATGGCGAT GCTGCTTGC CGAATATCAT GGTGAAAT
 TGGCTTGAC AAGCGTCCG AGTTCGCGC GTACGGGTG CCGCTCCTAG AGCAGCACTG AGTACCGTA CCGACGAAAG GCTTATAGTA CCACCTTTTA
 G R F S G F I D C G R L G V A D R Y Q D I A L A T R D I A E E L G G .
 601 GCGCGCTTT CTGATTCAT CGACTGTGC CCGTGGGTG TGGCGGACCG CTATCAGGAC ATAGCGTTGG CTACCGTGA TATTGCTGAA GAGCTTGGCG
 CCGGCGAAA GACCTAAGTA GGTGACACG GCCGACCCAC ACCGCTGCG GATAGTCTG TATCGCAAC GATGGCACT ATAAGCACTT CTCGAACCGC
 . E W A D R F L V L Y G I A A P D S Q R I A F Y R L L D E F F *
 701 GCGATGGC TGACCGCTC CTGTGCTTT ACGGTATGC CGCTCCGAT TCGAGCGCA TCGCTTCTA TCGCTTCT GACGAGTTCT TCTGA
 CGCTTACCG ACTGGGAG GAGCAGGAA TGCCATAGC GCGAGGCTA ACGTGGGT ACGGAGAT AGCGGAGAA CTGCTCAAGA AGACT

Figure 3

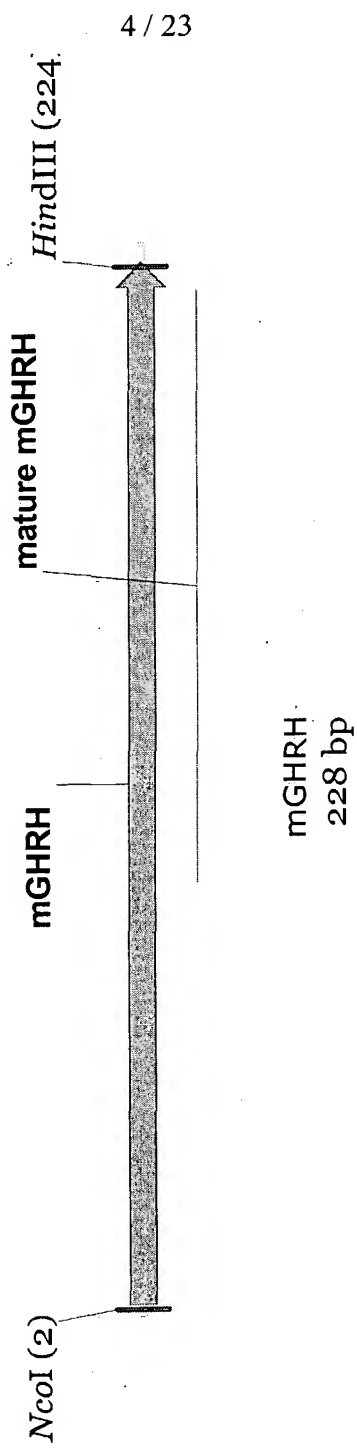


Figure 4

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+3 A M V L W V L F V I L I L T S G S H C S L P P S P P F R M Q R H V
1 GCCATGGTGC TCTGGGTGCT CTTGTGATC CTCATCCTCA CCAGGGGAG CCACTGCAGC CTGCCTCCCA GCCCTCCCTT CAGGATGCAG AGGCACGTGG
  CGGTACCACG AGACCCACGA GAAACACTAG GAGTAGGAGT GGTGGCCGTC GGTGACGTCG GACGGAGGGT CGGGAGGAA GTCCCTACGTC TCCGTGCACC

+3 D A I F T T N Y R K L L S Q L Y A R K V I Q D I M N K Q G E R I Q E
101 ACGCCATCTT CACCACCAAC TACAGGAAGC TGCTGAGCCA GTGTAGGCC AGGAAGGTGA TCCAGGACAT CATGAACAAG CAGGGCGAGA GGATCCAGGA
  TCGGGTAGAA GTGGTGGTTG ATGTCCTTCG ACGACTCGT CGACATCGG TCCTTCCACT AGTCCCTGTA GTACTTGTC GTCCCGCTCT CCTAGGTCCT

+3 Q R A R L S & # A C
201 GCAGAGGGCC AGGCTGAGT GATAAGCTTG C
  CGTCTCCCGG TCCGACTCGA CTATTGGAAC G
```

Figure 5

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GHRH-m Ori . CCATGGTGCTCTGGGTGCTCTTTTGTGATCCTCATCCTCACCAGTGGCTCCCACTGCTCA 60
|||||
GHRH-m Opt GCCATGGTGCTCTGGGTGCTCTTTTGTGATCCTCATCCTCACCAGCGGCAGGCCCACTGCAGC

GHRH-m Ori CTGCCCCCCTCACCTCCCTTCAGGATGCAGCGACACGTGGACGCCCATCTTCACCCACCAAC 120
|||||
GHRH-m Opt CTGCCCTCCCAAGCCCTCCCTTCAGGATGCAGAGGCACGTGGACGCCCATCTTCACCCACCAAC

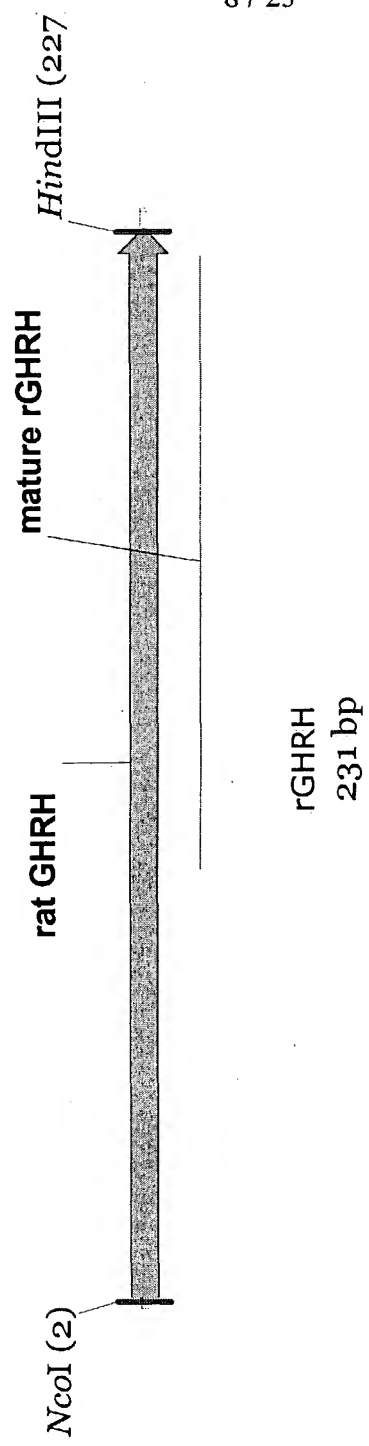
GHRH-m Ori TACAGGAAGCTGTGAGCCAGCTGTACGCCAGGAAGGTGATCCAGGACATCATGAACAAG 180
|||||
GHRH-m Opt TACAGGAAGCTGTGAGCCAGCTGTACGCCAGGAAGGTGATCCAGGACATCATGAACAAG

GHRH-m Ori CAGGGCGAGAGAATCCAGGAGCAGAGGCCAGGCTGAGCTGATAAGCTT.. 231
|||||
GHRH-m Opt CAGGGCGAGAGGATCCAGGAGCAGAGGCCAGGCTGAGCTGATAAGCTTGC
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Figure 6

GHRH-M Ori .MVLWVLFVILLITSGSHCSLPPSPFFRMQRHVDAIFTTNYRKLLSQLYARKV IQDIMNK 60
|||||
GHRH-M opti AMVLWVLFVILLITSGSHCSLPPSPFFRMQRHVDAIFTTNYRKLLSQLYARKV IQDIMNK
GHRH-M Ori QGERIQEQARLSA. 75
|||||
GHRH-M opti QGERIQEQARLSAC

Figure 7



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Figure 8

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+3 A M A L W V F F V L L T L T S G S H C S L P P S P P F R V R R H A
1  GCCATGCCC TGTGGTGT CTTGGTCTG CTGACCTGA CCAGCGAAG CCACTGCAGC CTGCTCCCA GCCCTCCCT CAGGTGGC CGGCACGCC
   CGGTACCGG ACACCACAA GAAGCAGAC GACTGGGACT GGTGCTTC GGTGACGTC GACGGAGGT CGGAGGAA GTCCACGC GCCGTGCGC
+3 D A I F T S S Y R R I L G Q L Y A R K L L H E I M N R Q Q G E R N Q
101 ACGCATCTT CACGAGC TACAGGAGGA TCCTGGGCCA GCTGTACGCT AGGAAGTCC TGCACGAGAT CATGACAGG CAGCAGGGG AGAGGACCA
    TGGGTAGAA GTGGTCTCG ATGCTCTCT AGGACCGGT CGACATCGA TCCTTCGAGG ACGTGCTCTA GTACTTCTC GTGTCGCC TCTCTTGGT
+3 E Q R S R F N & # A C
201 GGACGAGG AGCAGGTTCA ACTGATAAGC TTGC
    CCTGCTCTC TGTCCAAGT TGACTATTG AACG

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Figure 9

GHRH-R Ori GCCATGGCACTCTGGGTGTTCTTTGTGCTCCTCACCCCTCACAGTGGCTCCCACTGCTCA 60
||||| ||| ||||||| ||||| ||| ||||| ||| ||||| |||
GHRH-R opti GCCATGGCCCTGTGGTGTTCTTCGTGCTGCTGACCCCTGACAGCGGAAAGCCCACTGCAGC
GHRH-R Ori CTGCCCCCCTCACCTCCCTTCAGGGTGCGGGCGGCA CGCCGACGCCCATCTTCACCCAGCAGC 120
||||| ||| ||||||| ||||| ||| ||||||| ||||| ||| ||||||| ||||| |||
GHRH-R opti CTGCCTCCCAGCCCTCCCTTCAGGGTGCGCGGGCA CGCCGACGCCCATCTTCACCCAGCAGC
GHRH-R Ori TACAGGAGAAATCCTGGGCCAGCTGTACGCCAGGAAACTGTGCACGACATCATGAACAGG 180
||||| ||| ||||||| ||||| ||| ||||| ||| ||||||| ||||| |||
GHRH-R opti TACAGGAGGATCCTGGGCCAGCTGTACGCTAGGAAAGCTCCTGCACGACATCATGAACAGG
GHRH-R Ori CAGCAGGGCGAGAGGAAC CAGGAGCAGAGGTCCAGGTTCAACTGATAAGCTTGC 234
||||| ||| ||||||| ||||| ||| ||||| ||| ||||||| ||||| |||
GHRH-R opti CAGCAGGGCGAGAGGAAC CAGGAGCAGAGGAGCAGGTTCAACTGATAAGCTTGC

Figure 10

GHRH-R Ori	.MALWVFFVLLTLTSGSHCSLPPSPPPFRVRRRHADAIFTSSYRRILGQLYARKLLHEIMNR	60
GHRH-R opti	AMALWVFFVLLTLTSGSHCSLPPSPPPFRVRRRHADAIFTSSYRRILGQLYARKLLHEIMNR	
GHRH-R Ori	QQGERNQEQRSRFNA.	76
GHRH-R opti	QQGERNQEQRSRFNAC	

Figure 11

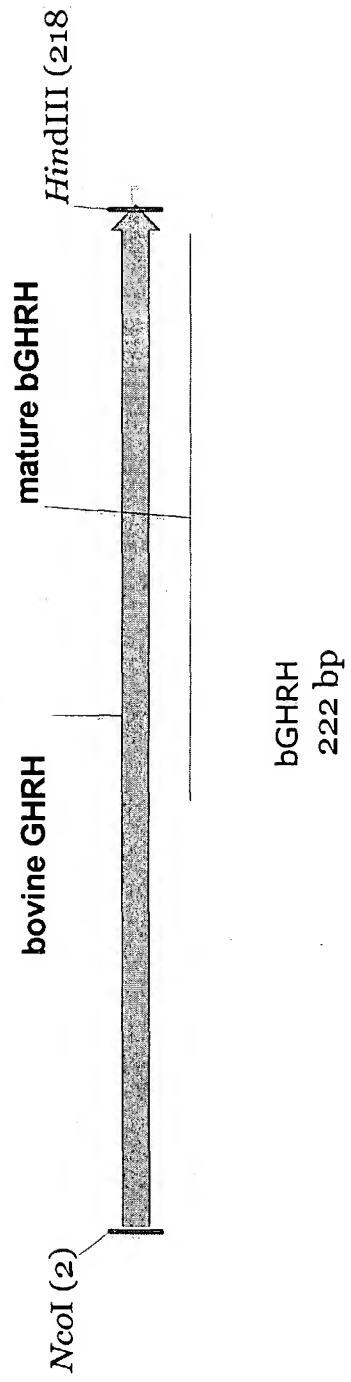


Figure 12

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+3 A M V L W V F F L V T L T L S S G S H G S L P S Q P L R I P R Y A
1  GCCATGGTGC TGTGGGTGT CTTCTGGTG ACCGTGACCC TGAGCAGCGG CTCCACGGC TCCCTGCCCT CCCAGCCTCT GCGATCCCT CGCTACGCCG
   CCGTACCACG ACACCCACAA GAAGGACCAC TGGGACTGGG ACTCGTCGCC GAGGGTGCCG AGGACGGGA GGTTCGGAGA CGCGTAGGGA GCGATGGGGC

+3 D A I F T N S Y R K V L G Q L S A R K L L Q D I M N R Q Q G E R N Q
101 ACGCCATCTT CACCAACAGC TACCGAAGG TGCTGGCCA GCTCAGGCC CGCAAGTCC TGCAGACAT CATGAACCGG CAGCAGGGCG AGCGCAACCA
   TCGGATAGAA GTGTTGTGCG ATGGCGTTCC ACGAGCCGGT CGAGTCGGG GCCTTCGAGG ACGTCTGTA GTACTTGCCG CTCGTCCCGC TCGCGTTGGT

+3 E Q G A & # A C
201 GGAGCAGGGA GCCTGATAAG CTTGC
   CCTCGTCCCT CGGACTATTC GAACG

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Figure 13

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GHRH-B Ori .CCATGGTGCTCTGGGTGTTCTTCTCGTGACCCCTCACCCCTCAGCAGCGGCTCCCAACGGT 60
|||||
GHRH-B opti GCCATGGTGCTGTGGGTGTTCTTCTCGTGACCCCTGACCCCTGAGCAGCGGCTCCCAACGGC
|||||

GHRH-B Ori TCCCTGCCCTTCCCAGCCTCTCAGGATTCACGGTACGCCGACGCCATCTTCACCAACAGC 120
|||||
GHRH-B opti TCCCTGCCCTCCCAGCCTCTGCGCATCCCTCGCTACGCCGACGCCATCTTCACCAACAGC
|||||

GHRH-B Ori TACCGGAAGGTGTGGGCCAGCTGTCCGCCCGGAAGCTGTGCAGGACATCATGAACAGG 180
|||||
GHRH-B opti TACCGCAAGGTGTGGGCCAGCTCAGCGCCCCGCAAGCTCCTGCAGGACATCATGAACCGG
|||||

GHRH-B Ori CAGCAGGGCGAGAGAAACCAGGAGCAGGGCGCCTGATAAGCTT.. 225
|||||
GHRH-B opti CAGCAGGGCGAGCGCAACCAGGAGCAGGGAGCCTGATAAGCTTGC
|||||
```

Figure 14

60

GHRH-B Ori .MVLWVFFLVTLTLSSGSHGSLPSQPLRIPRYADAIFTNSYRKVLGQLSARKLLQDIMNR
|||||
GHRH-B opti AMVLWVFFLVTLTLSSGSHGSLPSQPLRIPRYADAIFTNSYRKVLGQLSARKLLQDIMNR

73

GHRH-B Ori QQGERNQEQGAA.
|||||
GHRH-B opti QQGERNQEQGAAC

Figure 15

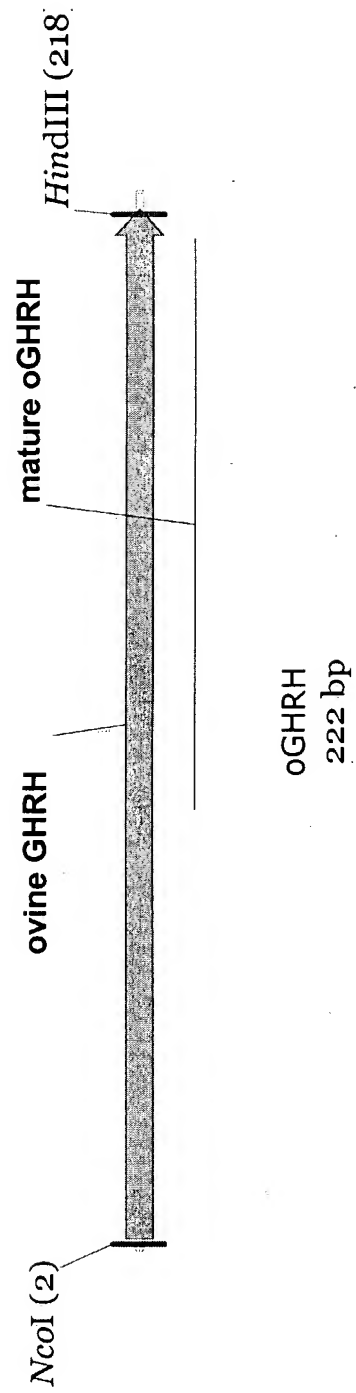


Figure 16

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+3 A M V L W V F F L V T L T L S S G S H G S L P S Q P L R I P R Y A
1 GCATGGTGC TGTGGTGT CTTCTGGTG ACCCTGACCC TGAGCAGCGG AGCCACGGC AGCCTGCCCA GCCAGCCCCT GAGGATCCCT AGGTACGCCG
  CGGTACCACG ACACCACAA GAAGGACCAC TGGGACTGGG ACTCGTCGC TCGGTGCCG TCGGACGGGT CGGTCCGGGA CTCCTAGGGA TCCATGCCGC

+3 D A I F T N S Y R K I L G Q L S A R K L L Q D I M N R Q Q G E R N Q
101 ACGCCATCTT CACCAACAGC TACAGGAAGA TCCTGGGCA GCTGAGCGCT AGGAAGCTCC TGCAGGACAT CATGAACAGG CAGCAGGGCG AGAGGAACCA
  TCGGCTAGAA GTGGTGTG ATGTCCTTCT AGGACCCGGT CGACTCGGA TCCTTCGAGG ACGTCCCTGTA GTACTGTCC GTCGTCCCGC TCTCCTTGGT

+3 E Q G A & # A C
201 GGAGCAGGGC GCCTGATAAG CTTGC
  CCTCGTCCCG CGGACTATTC GAACG

```

Figure 17

GHRH-O Ori . CCATGGTGCTCTGGGTGTTCTTCCTCGTGACCCCTCACCCCTCAGCAGCGGCTCCACGGT 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GHRH-O opti GCCATGGTGCTGTGGGTGTTCTTCCTGGTGACCCCTGACCCCTGAGCAGCGGAAGCCACGGC

 GHRH-O Ori TCCCTGCCCTTCCCAGCCCTCTCAGGATTCCACGGTACGCCGACGCCATCTTCACCAACAGC 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GHRH-O opti AGCCTGCCCCAGCCAGCCCCCTGAGGATCCCTAGGTACGCCGACGCCATCTTCACCAACAGC

 GHRH-O Ori TACCGGAAGATCCTGGGCCAGCTGTCCGCCCGGAAGCTGCTGCAGGACATCATGAACAGG 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GHRH-O opti TACAGGAAGATCCTGGGCCAGCTGAGCGCTAGGAAGCTCCTGCAGGACATCATGAACAGG

 GHRH-O Ori CAGCAGGGCGAGAGAAACCAGGAGCAGGGCGCCTGATAAGCTT... 225
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 GHRH-O opti CAGCAGGGCGAGAGGAACCAGGAGCAGGGCGCCTGATAAGCTTGC

Figure 18

GHRH-O Ori	.MVLWVFFLVTLTLSSCGSHGSLPSQPLRIPRYADAIFTNSYRKILGQLSARKLLQDIMNR	60
GHRH-O opti	AMVLWVFFLVTLTLSSCGSHGSLPSQPLRIPRYADAIFTNSYRKILGQLSARKLLQDIMNR	
GHRH-O Ori	QQGERNQEQGAA.	73
GHRH-O opti	QQGERNQEQGAAC	

Figure 19

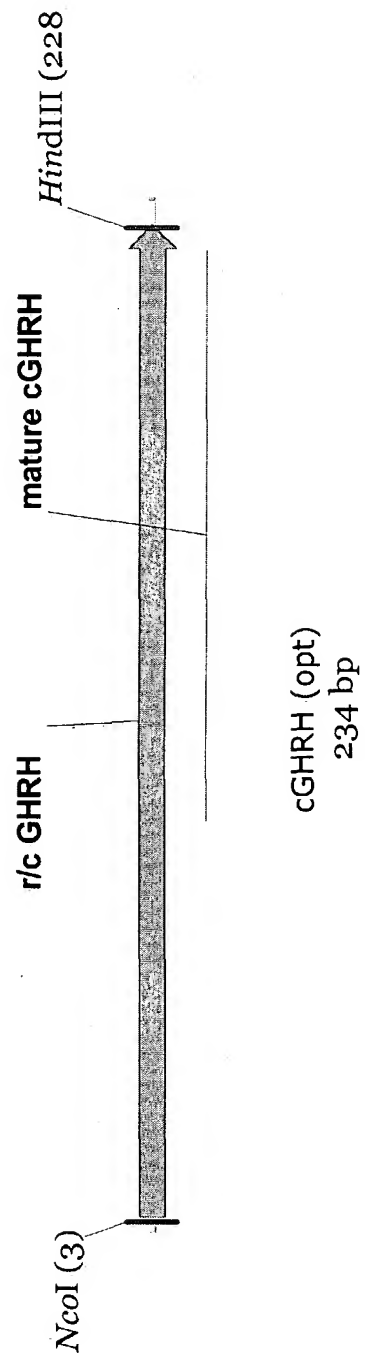


Figure 20

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+3 A M A L W V F F V L L T L T S G S H C S L P P S P P F R V R R H A
1  GCCATGGCCC TGTGGTGT CTTGTGCTG CTGACCCCTGA CCTCCGGAAG CCACTGCAGC CTGCCACCA GCCCACCTT CCGGTCAGG CGCCACGCCG
CGGTACCGGG ACACCACAA GAACACGAC GACTGGGACT GGAGCCCTTC GGTGACGTCG GACGGTGGT CCGGTGGAA GCGCAGTCC GCGTGGGGC

+3 D G I F S K A Y R K L L G Q L S A R N Y L H S L M A K R V G S G L G
101 ACGGCATCTT CAGCAAGGCC TACGCAAGC TCCTGGGCCA GCTGAGCGCA CGCAACTACC TGCACAGCT GATGGCAAG CCGTGGGCA GCGGACTGGG
TGCCGTAGAA GTCGTTCCGG ATGGCGTTG AGGACCCGGT CGACTCGCGT GCGTTGATGG ACGTGTGGA CTACCGGTT CCGCACCCGT CGCCTGACCC

+3 D E A E P L S & # A C
201 AGACGAGGCC GAGCCCTGA GCTGATAAGC TTGC
TCTGCTCCGG CTCGGGACT CGACTATTG AACG

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Figure 21

Figure 22

60

GHRH /ori .MALWVFFVLLTLTSGSHCSLPPSPFFRVRRHADGIFSKAYRKLLGQLSARNYLHSLMAK
o|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GHRH/opt-Chi AMALWVFFVLLTLTSGSHCSLPPSPFFRVRRHADGIFSKAYRKLLGQLSARNYLHSLMAK

76

GHRH /ori RVGSGLGDEAEPLSA.
|o|||||||||||||o
GHRH/opt-Chi RVGSGLGDEAEPLSAC

Figure 23